

## SEQUENCE LISTING

<110> Prof. Dr. Werner Seeger  
 <120> Novel chimeric plasminogen activators and their pharmaceutical use  
 <160> 13

<210> 1  
 <211> 1143  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1) ... (1143)  
 <223> Coding sequence of the surfactant protein B precursor

<400> 1

atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ccc acg	48
Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr	
1 5 10 15	
ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt	96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys	
20 25 30	
gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag	144
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln	
35 40 45	
tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga	192
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly	
50 55 60	
gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac	240
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn	
65 70 75 80	
aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg	288
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu	
85 90 95	
gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc	336
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys	
100 105 110	
aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag	384
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln	
115 120 125	
aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa	432
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys	
130 135 140	
tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg	480
Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu	
145 150 155 160	
ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc	528

Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu	
165 170 175	
gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac	576
Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His	
180 185 190	
aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc	624
Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys	
195 200 205	
tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag	672
Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys	
210 215 220	
ggc gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg	720
Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu	
225 230 235 240	
gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc	768
Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile	
245 250 255	
ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc	816
Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg	
260 265 270	
ctc gtc ctc cgg tgc tcc atg gat gac agc gct ggc cca agg tcg ccg	864
Leu Val Leu Arg Cys Ser Met Asp Asp Ser Ala Gly Pro Arg Ser Pro	
275 280 285	
aca gga gaa tgg ctg ccg cga gac tct gag tgc cac ctc tgc atg tcc	912
Thr Gly Glu Trp Leu Pro Arg Asp Ser Glu Cys His Leu Cys Met Ser	
290 295 300	
gtg acc acc cag gcc ggg aac agc agc gag cag gcc ata cca cag gca	960
Val Thr Thr Gln Ala Gly Asn Ser Ser Glu Gln Ala Ile Pro Gln Ala	
305 310 315 320	
atg ctc cag gcc tgt gtt ggc tcc tgg ctg gac agg gaa aag tgc aag	1008
Met Leu Gln Ala Cys Val Gly Ser Trp Leu Asp Arg Glu Lys Cys Lys	
325 330 335	
caa ttt gtg gag cag cac acg ccc cag ctg ctg acc ctg gtg ccc agg	1056
Gln Phe Val Glu Gln His Thr Pro Gln Leu Leu Thr Leu Val Pro Arg	
340 345 350	
ggc tgg gat gcc cac acc acc tgc cag gcc ctc ggg gtg tgt ggg acc	1104
Gly Trp Asp Ala His Thr Thr Cys Gln Ala Leu Gly Val Cys Gly Thr	
355 360 365	
atg tcc agc cct ctc cag tgt atc cac agc ccc gac ctt	1143
Met Ser Ser Pro Leu Gln Cys Ile His Ser Pro Asp Leu	
370 375 380	

&lt;210&gt; 2

&lt;211&gt; 837

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) ... (837)

&lt;223&gt; Coding sequence of the surfactant protein B precursor lacking the C-terminal propeptide

&lt;400&gt; 2

atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ccc acg	48
Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr	
1 5 10 15	
ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt	96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys	
20 25 30	
gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag	144
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln	
35 40 45	
tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga	192
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly	
50 55 60	
gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac	240
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn	
65 70 75 80	
aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg	288
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu	
85 90 95	
gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc	336
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys	
100 105 110	
aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag	384
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln	
115 120 125	
aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa	432
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys	
130 135 140	
tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg	480
Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu	
145 150 155 160	
ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc	528
Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu	
165 170 175	
gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac	576
Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His	
180 185 190	
aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc	624

Thr	Gln	Asp	Leu	Ser	Glu	Gln	Gln	Phe	Pro	Ile	Pro	Leu	Pro	Tyr	Cys		
		195					200					205					
tgg	ctc	tgc	agg	gct	ctg	atc	aag	cgg	atc	caa	gcc	atg	att	ccc	aag		672
Trp	Leu	Cys	Arg	Ala	Leu	Ile	Lys	Arg	Ile	Gln	Ala	Met	Ile	Pro	Lys		
	210					215				220							
ggt	gcg	cta	gct	gtg	gca	gtg	gcc	cag	gtg	tgc	cgc	gtg	gta	cct	ctg		720
Gly	Ala	Leu	Ala	Val	Ala	Val	Ala	Gln	Val	Cys	Arg	Val	Val	Pro	Leu		
225					230				235					240			
gtg	gcg	ggc	ggc	atc	tgc	cag	tgc	ctg	gct	gag	cgc	tac	tcc	gtc	atc		768
Val	Ala	Gly	Gly	Ile	Cys	Gln	Cys	Leu	Ala	Glu	Arg	Tyr	Ser	Val	Ile		
				245				250						255			
ctg	ctc	gac	acg	ctg	ctg	ggc	cgc	atg	ctg	ccc	cag	ctg	gtc	tgc	cgc		816
Leu	Leu	Asp	Thr	Leu	Leu	Gly	Arg	Met	Leu	Pro	Gln	Leu	Val	Cys	Arg		
			260					265					270				
ctc	gtc	ctc	cgg	tgc	tcc	atg											837
Leu	Val	Leu	Arg	Cys	Ser	Met											
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<210> 3  
 <211> 237  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1) ... (237)  
 <223> Coding sequence of the mature surfactant protein B

<400> 3

ttc	ccc	att	cct	ctc	ccc	tat	tgc	tgg	ctc	tgc	agg	gct	ctg	atc	aag		48
Phe	Pro	Ile	Pro	Leu	Pro	Tyr	Cys	Trp	Leu	Cys	Arg	Ala	Leu	Ile	Lys		
1				5				10						15			
cgg	atc	caa	gcc	atg	att	ccc	aag	ggt	gcg	cta	gct	gtg	gca	gtg	gcc		96
Arg	Ile	Gln	Ala	Met	Ile	Pro	Lys	Gly	Ala	Leu	Ala	Val	Ala	Val	Ala		
			20					25					30				
cag	gtg	tgc	cgc	gtg	gta	cct	ctg	gtg	gcg	ggc	ggc	atc	tgc	cag	tgc		144
Gln	Val	Cys	Arg	Val	Val	Pro	Leu	Val	Ala	Gly	Gly	Ile	Cys	Gln	Cys		
			35				40					45					
ctg	gct	gag	cgc	tac	tcc	gtc	atc	ctg	ctc	gac	acg	ctg	ctg	ggc	cgc		192
Leu	Ala	Glu	Arg	Tyr	Ser	Val	Ile	Leu	Leu	Asp	Thr	Leu	Leu	Gly	Arg		
	50					55				60							
atg	ctg	ccc	cag	ctg	gtc	tgc	cgc	ctc	gtc	ctc	cgg	tgc	tcc	atg			237
Met	Leu	Pro	Gln	Leu	Val	Cys	Arg	Leu	Val	Leu	Arg	Cys	Ser	Met			
65				70						75							

<210> 4  
 <211> 1293

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) ... (1293)

&lt;223&gt; Coding sequence of the single-chain urokinase-plasminogen activator

&lt;400&gt; 4

atg aga gcc ctg ctg gcg cgc ctg ctt ctc tgc gtc ctg gtc gtg agc	48
Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser	
1 5 10 15	
gac tcc aaa ggc agc aat gaa ctt cat caa gtt cca tcg aac tgt gac	96
Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp	
20 25 30	
tgt cta aat gga gga aca tgt gtg tcc aac aag tac ttc tcc aac att	144
Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile	
35 40 45	
cac tgg tgc aac tgc cca aag aaa ttc gga ggg cag cac tgt gaa ata	192
His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile	
50 55 60	
gat aag tca aaa acc tgc tat gag ggg aat ggt cac ttt tac cga gga	240
Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly	
65 70 75 80	
aag gcc agc act gac acc atg ggc cgg ccc tgc ctg ccc tgg aac tct	288
Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser	
85 90 95	
gcc act gtc ctt cag caa acg tac cat gcc cac aga tct gat gct ctt	336
Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu	
100 105 110	
cag ctg ggc ctg ggg aaa cat aat tac tgc agg aac cca gac aac cgg	384
Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg	
115 120 125	
agg cga ccc tgg tgc tat gtg cag gtg ggc cta aag ccg ctt gtc caa	432
Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln	
130 135 140	
gag tgc atg gtg cat gac tgc gca gat gga aaa aag ccc tcc tct cct	480
Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro	
145 150 155 160	
cca gaa gaa tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc	528
Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg	
165 170 175	
ttt aag att att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg	576
Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp	
180 185 190	
ttt gcg gcc atc tac agg agg cac cgg ggg ggc tct gtc acc tac gtg	624

Phe	Ala	Ala	Ile	Tyr	Arg	Arg	His	Arg	Gly	Gly	Ser	Val	Thr	Tyr	Val	
	195						200					205				
tgt	gga	ggc	agc	ctc	atc	agc	cct	tgc	tgg	gtg	atc	agc	gcc	aca	cac	672
Cys	Gly	Gly	Ser	Leu	Ile	Ser	Pro	Cys	Trp	Val	Ile	Ser	Ala	Thr	His	
	210						215				220					
tgc	ttc	att	gat	tac	cca	aag	aag	gag	gac	tac	atc	gtc	tac	ctg	ggc	720
Cys	Phe	Ile	Asp	Tyr	Pro	Lys	Lys	Glu	Asp	Tyr	Ile	Val	Tyr	Leu	Gly	
225					230					235					240	
cgc	tca	agg	ctt	aac	tcc	aac	acg	caa	ggg	gag	atg	aag	ttt	gag	gtg	768
Arg	Ser	Arg	Leu	Asn	Ser	Asn	Thr	Gln	Gly	Glu	Met	Lys	Phe	Glu	Val	
				245					250					255		
gaa	aac	ctc	atc	cta	cac	aag	gac	tac	agc	gct	gac	acg	ctt	gct	cac	816
Glu	Asn	Leu	Ile	Leu	His	Lys	Asp	Tyr	Ser	Ala	Asp	Thr	Leu	Ala	His	
		260						265					270			
cac	aac	gac	att	gcc	ttg	ctg	aag	atc	cgt	tcc	aag	gag	ggc	agg	tgt	864
His	Asn	Asp	Ile	Ala	Leu	Leu	Lys	Ile	Arg	Ser	Lys	Glu	Gly	Arg	Cys	
		275					280					285				
gcg	cag	cca	tcc	cgg	act	ata	cag	acc	atc	tgc	ctg	ccc	tcg	atg	tat	912
Ala	Gln	Pro	Ser	Arg	Thr	Ile	Gln	Thr	Ile	Cys	Leu	Pro	Ser	Met	Tyr	
	290					295					300					
aac	gat	ccc	cag	ttt	ggc	aca	agc	tgt	gag	atc	act	ggc	ttt	gga	aaa	960
Asn	Asp	Pro	Gln	Phe	Gly	Thr	Ser	Cys	Glu	Ile	Thr	Gly	Phe	Gly	Lys	
305					310					315				320		
gag	aat	tct	acc	gac	tat	ctc	tat	ccg	gag	cag	ctg	aaa	atg	act	gtt	1008
Glu	Asn	Ser	Thr	Asp	Tyr	Leu	Tyr	Pro	Glu	Gln	Leu	Lys	Met	Thr	Val	
				325					330					335		
gtg	aag	ctg	att	tcc	cac	cgg	gag	tgt	cag	cag	ccc	cac	tac	tac	ggc	1056
Val	Lys	Leu	Ile	Ser	His	Arg	Glu	Cys	Gln	Gln	Pro	His	Tyr	Tyr	Gly	
			340					345					350			
tct	gaa	gtc	acc	acc	aaa	atg	ctg	tgt	gct	gct	gac	cca	cag	tgg	aaa	1104
Ser	Glu	Val	Thr	Thr	Lys	Met	Leu	Cys	Ala	Ala	Asp	Pro	Gln	Trp	Lys	
		355					360					365				
aca	gat	tcc	tgc	cag	gga	gac	tca	ggg	gga	ccc	ctc	gtc	tgt	tcc	ctc	1152
Thr	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Ser	Leu	
	370					375					380					
caa	ggc	cgc	atg	act	ttg	act	gga	att	gtg	agc	tgg	ggc	cgt	gga	tgt	1200
Gln	Gly	Arg	Met	Thr	Leu	Thr	Gly	Ile	Val	Ser	Trp	Gly	Arg	Gly	Cys	
385					390					395					400	
gcc	ctg	aag	gac	aag	cca	ggc	gtc	tac	acg	aga	gtc	tca	cac	ttc	tta	1248
Ala	Leu	Lys	Asp	Lys	Pro	Gly	Val	Tyr	Thr	Arg	Val	Ser	His	Phe	Leu	
				405					410					415		
ccc	tgg	atc	cgc	agt	cac	acc	aag	gaa	gag	aat	ggc	ctg	gcc	ctc		1293
Pro	Trp	Ile	Arg	Ser	His	Thr	Lys	Glu	Gln	Asn	Gly	Leu	Ala	Leu		
			420					425					430			



<210> 5  
 <211> 828  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> CDS  
 <222> (1) ... (828)  
 <223> Coding sequence of the low molecular weight two-chain urokinase-plasminogen activator

<400> 5

aag ccc tcc tct cct cca gaa gaa tta aaa ttt cag tgt ggc caa aag	48
Lys Pro Ser Ser Pro Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys	
1 5 10 15	
act ctg agg ccc cgc ttt aag att att ggg gga gaa ttc acc acc atc	96
Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile	
20 25 30	
gag aac cag ccc tgg ttt gcg gcc atc tac agg agg cac cgg ggg ggc	144
Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly	
35 40 45	
tct gtc acc tac gtg tgt gga ggc agc ctc atc agc cct tgc tgg gtg	192
Ser Val Thr Tyr Val Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val	
50 55 60	
atc agc gcc aca cac tgc ttc att gat tac cca aag aag gag gac tac	240
Ile Ser Ala Thr His Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr	
65 70 75 80	
atc gtc tac ctg ggt cgc tca agg ctt aac tcc aac acg caa ggg gag	288
Ile Val Tyr Leu Gly Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu	
85 90 95	
atg aag ttt gag gtg gaa aac ctc atc cta cac aag gac tac agc gct	336
Met Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala	
100 105 110	
gac acg ctt gct cac cac aac gac att gcc ttg ctg aag atc cgt tcc	384
Asp Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser	
115 120 125	
aag gag ggc agg tgt gcg cag cca tcc cgg act ata cag acc atc tgc	432
Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys	
130 135 140	
ctg ccc tcg atg tat aac gat ccc cag ttt ggc aca agc tgt gag atc	480
Leu Pro Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile	
145 150 155 160	
act ggc ttt gga aaa gag aat tct acc gac tat ctc tat ccg gag cag	528
Thr Gly Phe Gly Lys Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln	
165 170 175	
ctg aaa atg act gtt gtg aag ctg att tcc cac cgg gag tgt cag cag	576

Leu Lys Met Thr Val Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln  
 180 185 190  
 ccc cac tac tac ggc tct gaa gtc acc acc aaa atg ctg tgt gct gct 624  
 Pro His Tyr Tyr Gly Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala  
 195 200 205  
 gac cca cag tgg aaa aca gat tcc tgc cag gga gac tca ggg gga ccc 672  
 Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro  
 210 215 220  
 ctc gtc tgt tcc ctc caa ggc cgc atg act ttg act gga att gtg agc 720  
 Leu Val Cys Ser Leu Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser  
 225 230 235 240  
 tgg ggc cgt gga tgt gcc ctg aag gac aag cca ggc gtc tac acg aga 768  
 Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg  
 245 250 255  
 gtc tca cac ttc tta ccc tgg atc cgc agt cac acc aag gaa gag aat 816  
 Val Ser His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Gln Asn  
 260 265 270  
 ggc ctg gcc ctc 828  
 Gly Leu Ala Leu  
 275

&lt;210&gt; 6

&lt;211&gt; 1671

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) ... (837)

&lt;223&gt; Coding sequence of the surfactant protein B precursor lacking the C-terminal propeptide

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (844) ... (1671)

&lt;223&gt; Coding sequence of the low molecular weight two-chain urokinase-plasminogen activator

&lt;400&gt; 6

atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ctg ccc acg 48  
 Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr  
 1 5 10 15  
 ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt 96  
 Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys  
 20 25 30  
 gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag 144  
 Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln  
 35 40 45



tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly 50 55 60	192
gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn 65 70 75 80	240
aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu 85 90 95	288
gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys 100 105 110	336
aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln 115 120 125	384
aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys 130 135 140	432
tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu 145 150 155 160	480
ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu 165 170 175	528
gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His 180 185 190	576
aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys 195 200 205	624
tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys 210 215 220	672
ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu 225 230 235 240	720
gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile 245 250 255	768
ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg 260 265 270	816
ctc gtc ctc cgg tgc tcc atg aag ctt aag ccc tcc tct cct cca gaa Leu Val Leu Arg Cys Ser Met Lys Leu Lys Pro Ser Ser Pro Pro Glu 275 280 285	864

gaa tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc ttt aag Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys 290 295 300	912
att att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg ttt gcg Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala 305 310 315 320	960
gcc atc tac agg agg cac cgg ggg ggc tct gtc acc tac gtg tgt gga Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly 325 330 335	1008
ggc agc ctc atc agc cct tgc tgg gtg atc agc gcc aca cac tgc ttc Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe 340 345 350	1056
att gat tac cca aag aag gag gac tac atc gtc tac ctg ggt cgc tca Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser 355 360 365	1104
agg ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtg gaa aac Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn 370 375 380	1152
ctc atc cta cac aag gac tac agc gct gac acg ctt gct cac cac aac Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn 385 390 395 400	1200
gac att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt gcg cag Asp Ile Ala Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln 405 410 415	1248
cca tcc cgg act ata cag acc atc tgc ctg ccc tcg atg tat aac gat Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp 420 425 430	1296
ccc cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa gag aat Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn 435 440 445	1344
tct acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt gtg aag Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys 450 455 460	1392
ctg att tcc cac cgg gag tgt cag cag ccc cac tac tac ggc tct gaa Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu 465 470 475 480	1440
gtc acc acc aaa atg ctg tgt gct gct gac cca cag tgg aaa aca gat Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp 485 490 495	1488
tcc tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc caa ggc Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly 500 505 510	1536
cgc atg act ttg act gga att gtg agc tgg ggc cgt gga tgt gcc ctg Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu	1584

515 520 525

aag gac aag cca ggc gtc tac acg aga gtc tca cac ttc tta ccc tgg 1632  
 Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp  
 530 535 540

atc cgc agt cac acc aag gaa gag aat ggc ctg gcc ctc 1671  
 Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu  
 545 550 555

<210> 7  
 <211> 1674  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS  
 <222> (1) ... (837)  
 <223> Coding sequence of the surfactant protein B precursor lacking the C-terminal propeptide

<220>  
 <221> CDS  
 <222> (847) ... (1674)  
 <223> Coding sequence of the low molecular weight two-chain urokinase-plasminogen activator

<400> 7

atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ctg ccc acg 48  
 Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr  
 1 5 10 15

ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt 96  
 Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys  
 20 25 30

gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag 144  
 Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln  
 35 40 45

tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga 192  
 Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly  
 50 55 60

gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac 240  
 Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn  
 65 70 75 80

aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg 288  
 Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu  
 85 90 95

gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc 336  
 Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys  
 100 105 110

aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag 384

Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln	
115 120 125	
aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa	432
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys	
130 135 140	
tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg	480
Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu	
145 150 155 160	
ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc	528
Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu	
165 170 175	
gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac	576
Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His	
180 185 190	
aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc	624
Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys	
195 200 205	
tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag	672
Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys	
210 215 220	
ggg ggc cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg	720
Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu	
225 230 235 240	
gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc	768
Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile	
245 250 255	
ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc	816
Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg	
260 265 270	
ctc gtc ctc cgg tgc tcc atg cag ata tct aag ccc tcc tct cct cca	864
Leu Val Leu Arg Cys Ser Met Gln Ile Ser Lys Pro Ser Ser Pro Pro	
275 280 285	
gaa gaa tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc ttt	912
Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe	
290 295 300	
aag att att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg ttt	960
Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe	
305 310 315 320	
gcg gcc atc tac agg agg cac cgg ggg ggc tct gtc acc tac gtg tgt	1008
Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys	
325 330 335	
gga ggc agc ctc atc agc cct tgc tgg gtg atc agc gcc aca cac tgc	1056
Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys	
340 345 350	

ttc att gat tac cca aag aag gag gac tac atc gtc tac ctg ggt cgc 1104  
 Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg  
 355 360 365

tca agg ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtg gaa 1152  
 Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu  
 370 375 380

aac ctg atc cta cac aag gac tac agc gct gac acg ctt gct cac cac 1200  
 Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His  
 385 390 395 400

aac gac att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt gcg 1248  
 Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala  
 405 410 415

cag cca tcc cgg act ata cag acc atc tgc ctg ccc tcg atg tat aac 1296  
 Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn  
 420 425 430

gat ccc cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa gag 1344  
 Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu  
 435 440 445

aat tct acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt gtg 1392  
 Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val  
 450 455 460

aag ctg att tcc cac cgg gag tgt cag cag ccc cac tac tac ggc tct 1440  
 Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser  
 465 470 475 480

gaa gtc acc acc aaa atg ctg tgt gct gct gac cca cag tgg aaa aca 1488  
 Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr  
 485 490 495

gat tcc tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc caa 1536  
 Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln  
 500 505 510

ggc cgc atg act ttg act gga att gtg agc tgg ggc cgt gga tgt gcc 1584  
 Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala  
 515 520 525

ctg aag gac aag cca ggc gtc tac acg aga gtc tca cac ttc tta ccc 1632  
 Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro  
 530 535 540

tgg atc cgc agt cac acc aag gaa gag aat ggc ctg gcc ctc 1674  
 Trp Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu  
 545 550 555

&lt;210&gt; 8

&lt;211&gt; 591

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) ... (591)

&lt;223&gt; Coding sequence of the surfactant protein C precursor

&lt;400&gt; 8

atg gat gtg ggc agc aaa gag gtc ctg atg gag agc ccg ccg gac tac	48
Met Asp Val Gly Ser Lys Glu Val Leu Met Glu Ser Pro Pro Asp Tyr	
1 5 10 15	
tcc gca gct ccc cgg ggc cga ttt ggc att ccc tgc tgc cca gtg cac	96
Ser Ala Ala Pro Arg Gly Arg Phe Gly Ile Pro Cys Cys Pro Val His	
20 25 30	
ctg aaa cgc ctt ctt atc gtg gtg gtg gtg gtg gtc ctc atc gtc gtg	144
Leu Lys Arg Leu Leu Ile Val Val Val Val Val Val Leu Ile Val Val	
35 40 45	
gtg att gtg gga gcc ctg ctc atg ggt ctc cac atg agc cag aaa cac	192
Val Ile Val Gly Ala Leu Leu Met Gly Leu His Met Ser Gln Lys His	
50 55 60	
acg gag atg gtt ctg gag atg agc att ggg gcg ccg gaa gcc cag caa	240
Thr Glu Met Val Leu Glu Met Ser Ile Gly Ala Pro Glu Ala Gln Gln	
65 70 75 80	
cgc ctg gcc ctg agt gag cac ctg gtt acc act gcc acc ttc tcc atc	288
Arg Leu Ala Leu Ser Glu His Leu Val Thr Thr Ala Thr Phe Ser Ile	
85 90 95	
ggc tcc act ggc ctc gtg gtg tat gac tac cag cag ctg ctg atc gcc	336
Gly Ser Thr Gly Leu Val Val Tyr Asp Tyr Gln Gln Leu Leu Ile Ala	
100 105 110	
tac aag cca gcc cct ggc acc tgc tgc tac atc atg aag ata gct cca	384
Tyr Lys Pro Ala Pro Gly Thr Cys Cys Tyr Ile Met Lys Ile Ala Pro	
115 120 125	
gag agc atc ccc agt ctt gag gct ctc act aga aaa gtc cac aac ttc	432
Glu Ser Ile Pro Ser Leu Glu Ala Leu Thr Arg Lys Val His Asn Phe	
130 135 140	
cag atg gaa tgc tct ctg cag gcc aag ccc gca gtg cct acg tct aag	480
Gln Met Glu Cys Ser Leu Gln Ala Lys Pro Ala Val Pro Thr Ser Lys	
145 150 155 160	
ctg ggc cag gca gag ggg cga gat gca ggc tca gca ccc tcc gga ggg	528
Leu Gly Gln Ala Glu Gly Arg Asp Ala Gly Ser Ala Pro Ser Gly Gly	
165 170 175	
gac ccg gcc ttc ctg ggc atg gcc gtg agc acc ctg tgt ggc gag gtg	576
Asp Pro Ala Phe Leu Gly Met Ala Val Ser Thr Leu Cys Gly Glu Val	
180 185 190	
ccg ctc tac tac atc	591
Pro Leu Tyr Tyr Ile	
195	



<210> 9  
 <211> 174  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1) ... (174)  
 <223> Coding sequence of the surfactant protein C precursor lacking the C-terminal propeptide

<400> 9

atg gat gtg ggc agc aaa gag gtc ctg atg gag agc ccg ccg gac tac	48
Met Asp Val Gly Ser Lys Glu Val Leu Met Glu Ser Pro Pro Asp Tyr	
1 5 10 15	
tcc gca gct ccc cgg ggc cga ttt ggc att ccc tgc tgc cca gtg cac	96
Ser Ala Ala Pro Arg Gly Arg Phe Gly Ile Pro Cys Cys Pro Val His	
20 25 30	
ctg aaa cgc ctt ctt atc gtg gtg gtg gtg gtg gtc ctc atc gtc gtg	144
Leu Lys Arg Leu Leu Ile Val Val Val Val Val Val Leu Ile Val Val	
35 40 45	
gtg att gtg gga gcc ctg ctc atg ggt ctc	174
Val Ile Val Gly Ala Leu Leu Met Gly Leu	
50 55	

<210> 10  
 <211> 105  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1) ... (105)  
 <223> Coding sequence of the mature surfactant protein C

<400> 10

ttt ggc att ccc tgc tgc cca gtg cac ctg aaa cgc ctt ctt atc gtg	48
Phe Gly Ile Pro Cys Cys Pro Val His Leu Lys Arg Leu Leu Ile Val	
1 5 10 15	
gtg gtg gtg gtg gtc ctc atc gtc gtg gtg att gtg gga gcc ctg ctc	96
Val Val Val Val Val Leu Ile Val Val Val Ile Val Gly Ala Leu Leu	
20 25 30	
atg ggt ctc	105
Met Gly Leu	
35	

<210> 11  
 <211> 1686  
 <212> DNA  
 <213> Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) ... (1686)

&lt;223&gt; Coding sequence of the tissue-plasminogen activator

&lt;400&gt; 11

atg gat gca atg aag aga ggg ctc tgc tgt gtg ctg ctg ctg tgt gga	48
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly	
1 5 10 15	
gca gtc ttc gtt tcg ccc agc cag gaa atc cat gcc cga ttc aga aga	96
Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg	
20 25 30	
gga gcc aga tct tac caa gtg atc tgc aga gat gaa aaa acg cag atg	144
Gly Ala Arg Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met	
35 40 45	
ata tac cag caa cat cag tca tgg ctg cgc cct gtg ctc aga agc aac	192
Ile Tyr Gln Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn	
50 55 60	
cgg gtg gaa tat tgc tgg tgc aac agt ggc agg gca cag tgc cac tca	240
Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser	
65 70 75 80	
gtg cct gtc aaa agt tgc agc gag cca agg tgt ttc aac ggg ggc acc	288
Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr	
85 90 95	
tgc cag cag gcc ctg tac ttc tca gat ttc gtg tgc cag tgc ccc gaa	336
Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu	
100 105 110	
gga ttt gct ggg aag tgc tgt gaa ata gat acc agg gcc acg tgc tac	384
Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr	
115 120 125	
gag gac cag ggc atc agc tac agg ggc acg tgg agc aca gcg gag agt	432
Glu Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser	
130 135 140	
ggc gcc gag tgc acc aac tgg aac agc agc gcg ttg gcc cag aag ccc	480
Gly Ala Glu Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro	
145 150 160 165	
tac agc ggg cgg agg cca gat gcc atc agg ctg ggc ctg ggg aac cac	528
Tyr Ser Gly Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His	
170 175 180	
aac tac tgc aga aac cca gat cga gac tca aag ccc tgg tgc tac gtc	576
Asn Tyr Cys Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val	
185 190 195	
ttt aag gcg ggg aag tac agc tca gag ttc tgc agc acc cct gcc tgc	624
Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys	
200 205 205	

tct gag gga aac agt gac tgc tac ttt ggg aat ggg tca gcc tac cgt Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg 210 215 220	672
ggc acg cac agc ctc acc gag tcg ggt gcc tcc tgc ctc ccg tgg aat Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn 225 230 235 240	720
tcc atg atc ctg ata ggc aag gtt tac aca gca cag aac ccc agt gcc Ser Met Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala 245 250 255	768
cag gca ctg ggc ctg ggc aaa cat aat tac tgc cgg aat cct gat ggg Gln Ala Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly 260 265 270	816
gat gcc aag ccc tgg tgc cac gtg ctg aag aac cgc agg ctg acg tgg Asp Ala Lys Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp 275 280 285	864
gag tac tgt gat gtg ccc tcc tgc tcc acc tgc ggc ctg aga cag tac Glu Tyr Cys Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr 290 295 300	912
agc cag cct cag ttt cgc atc aaa gga ggg ctc ttc gcc gac atc gcc Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe Ala Asp Ile Ala 305 310 315 320	960
tcc cac ccc tgg cag gct gcc atc ttt gcc aag cac agg agg tcg ccc Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser Pro 325 330 335	1008
gga gag cgg ttc ctg tgc ggg ggc ata ctc atc agc tcc tgc tgg att Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile 340 345 350	1056
ctc tct gcc gcc cac tgc ttc cag gag agg ttt ccg ccc cac cac ctg Leu Ser Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu 355 360 365	1104
acg gtg atc ttg ggc aga aca tac cgg gtg gtc cct ggc gag gag gag Thr Val Ile Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu 370 375 380	1152
cag aaa ttt gaa gtc gaa aaa tac att gtc cat aag gaa ttc gat gat Gln Lys Phe Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp 385 390 395 400	1200
gac act tac gac aat gac att gcg ctg ctg cag ctg aaa tcg gat tcg Asp Thr Tyr Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser 405 410 415	1248
tcc cgc tgt gcc cag gag agc agc gtg gtc cgc act gtg tgc ctt ccc Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro 420 425 430	1296
ccg gcg gac ctg cag ctg ccg gac tgg acg gag tgt gag ctc tcc ggc Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly 435 440 445	1344

435	440	445	
tac ggc aag cat gag gcc ttg	tct cct ttc tat	tcg gag cgg ctg aag	1392
Tyr Gly Lys His Glu Ala Leu	Ser Pro Phe Tyr	Ser Glu Arg Leu Lys	
450	455	460	
gag gct cat gtc aga ctg tac	cca tcc agc cgc tgc aca tca caa cat		1440
Glu Ala His Val Arg Leu Tyr	Pro Ser Ser Arg Cys Thr Ser Gln His		
465	470	475	480
tta ctt aac aga aca gtc acc	gac aac atg ctg tgt gct gga gac act		1488
Leu Leu Asn Arg Thr Val Thr	Asp Asn Met Leu Cys Ala Gly Asp Thr		
	485	490	495
cgg agc ggc ggg ccc cag gca	aac ttg cac gac gcc tgc cag ggc gat		1536
Arg Ser Gly Gly Pro Gln Ala	Asn Leu His Asp Ala Cys Gln Gly Asp		
	500	505	510
tcg gga ggc ccc ctg gtg tgt	ctg aac gat ggc cgc atg act ttg gtg		1584
Ser Gly Gly Pro Leu Val Cys	Leu Asn Asp Gly Arg Met Thr Leu Val		
	515	520	525
ggc atc atc agc tgg ggc ctg	ggc tgt gga cag aag gat gtc ccg ggt		1632
Gly Ile Ile Ser Trp Gly Leu	Gly Cys Gly Gln Lys Asp Val Pro Gly		
	530	535	540
gtg tac acc aag gtt acc aac	tac cta gac tgg att cgt gac aac atg		1680
Val Tyr Thr Lys Val Thr Asn	Tyr Leu Asp Trp Ile Arg Asp Asn Met		
545	550	555	560
cga ccg			1686
Arg Pro			

<210> 12  
 <211> 1158  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> sig\_peptide  
 <222> (1) ... (69)  
 <223> Signal sequence of the surfactant protein B

<220>  
 <221> CDS  
 <222> (76) ... (312)  
 <223> Coding sequence of the mature surfactant protein B

<220>  
 <221> CDS  
 <222> (313) ... (1140)  
 <223> Coding sequence of the low molecular weight two-chain urokinase-plasminogen activator

<220>  
 <221> CDS  
 <222> (1141) ... (1158)  
 <223> Hexahistidin affinity tag

&lt;400&gt; 12

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Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr	
1 5 10 15	
ctc tgt ggc cca ggc act gct gcc tgg ttc ccc att cct ctc ccc tat	96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Phe Pro Ile Pro Leu Pro Tyr	
20 25 30	
tgc tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc	144
Cys Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro	
35 40 45	
aag ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct	192
Lys Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro	
50 55 60	
ctg gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc	240
Leu Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val	
65 70 75 80	
atc ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc	288
Ile Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys	
85 90 95	
cgc ctc gtc ctc cgg tgc tcc atg aag ccc tcc tct cct cca gaa gaa	336
Arg Leu Val Leu Arg Cys Ser Met Lys Pro Ser Ser Pro Pro Glu Glu	
100 105 110	
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Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile	
115 120 125	
att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg ttt gcg gcc	432
Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala	
130 135 140	
atc tac agg agg cac cgg ggg ggc tct gtc acc tac gtg tgt gga ggc	480
Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly	
145 150 155 160	
agc ctc atc agc cct tgc tgg gtg atc agc gcc aca cac tgc ttc att	528
Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile	
165 170 175	
gat tac cca aag aag gag gac tac atc gtc tac ctg ggt cgc tca agg	576
Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg	
180 185 190	
ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtg gaa aac ctc	624
Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu	
195 200 205	
atc cta cac aag gac tac agc gct gac acg ctt gct cac cac aac gac	672
Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp	
210 215 220	

att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt gcg cag cca	720
Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro	
225 230 235 240	
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Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro	
245 250 255	
cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa gag aat tct	816
Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser	
260 265 270	
acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt gtg aag ctg	864
Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu	
275 280 285	
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Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val	
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Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser	
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Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg	
325 330 335	
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Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys	
340 345 350	
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Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile	
355 360 365	
cgc agt cac acc aag gaa gag aat ggc ctg gcc ctc cat cat cat cat	1152
Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu His His His His	
370 375 380	
cat cat	1158
His His	
385	

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&lt;211&gt; 1149

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; sig\_peptide

&lt;222&gt; (1) ... (60)

&lt;223&gt; Signal sequence of the urokinase plasminogen activator

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (67) ... (894)



<223> Coding sequence of the low molecular weight two-chain urokinase-plasminogen activator

<220>

<221> CDS

<222> (895) ... (1131)

<223> Coding sequence of the mature surfactant protein B

<220>

<221> CDS

<222> (1132) ... (1149)

<223> Hexahistidin affinity tag

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Asp Ser Lys Gly Ser Asn Lys Pro Ser Ser Pro Pro Glu Glu Leu Lys	
20 25 30	
ttt cag tgt ggc caa aag act ctg agg ccc cgc ttt aag att att ggg	144
Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly	
35 40 45	
gga gaa ttc acc acc atc gag aac cag ccc tgg ttt gcg gcc atc tac	192
Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr	
50 55 60	
agg agg cac cgg ggg ggc tct gtc acc tac gtg tgt gga ggc agc ctc	240
Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser Leu	
65 70 75 80	
atc agc cct tgc tgg gtg atc agc gcc aca cac tgc ttc att gat tac	288
Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp Tyr	
85 90 95	
cca aag aag gag gac tac atc gtc tac ctg ggt cgc tca agg ctt aac	336
Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu Asn	
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tcc aac acg caa ggg gag atg aag ttt gag gtg gaa aac ctc atc cta	384
Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile Leu	
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His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile Ala	
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Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg	
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act ata cag acc atc tgc ctg ccc tcg atg tat aac gat ccc cag ttt	528
Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln Phe	
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ggc aca agc tgt gag atc act ggc ttt gga aaa gag aat tct acc gac	576
Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr Asp	
180 185 190	
tat ctc tat ccg gag cag ctg aaa atg act gtt gtg aag ctg att tcc	624
Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile Ser	
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Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln	
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Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met Thr	
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Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys	
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Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg Ser	
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His Thr Lys Glu Gln Asn Gly Leu Ala Leu Phe Pro Ile Pro Leu Pro	
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tgc cgc ctc gtc ctc cgg tgc tcc atg cat cat cat cat cat cat	1149
Cys Arg Leu Val Leu Arg Cys Ser Met His His His His His His	
370 375 380	